FIG. 1

Expression
Vector

Ap^R ori
             ON

lox

Promoter

lox   Gene of Interest

Univector
Construct

Kn^R OFF
         ori (conditional)

cre mediated lox-recombination
select for Km + Ap resistance

Promoter   lox   Gene of Interest

ori
ON

OFF
ori (conditional)

Kn^R

Ap^R lox

FIG. 2A

FIG. 2A. pUNI 10 (2220 bp) plasmid map showing restriction sites: HinD III (114), NotI (401), KpnI (409), EcoRI (452), XhoI (464), NdeI (472), NcoI (479), BamHI (485), NotI (489), HpaI (503), SalI (515), SacI (521), XbaI (750), EcoRV (890), BssHII (1335), PstI (1683), BglII (1896). Features: ori, lox, Poly A Site, TERM, Kan.

FIG. 2B

```
(401) NotI    KpnI    _____ LOX _____
GC GGC CGC GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TCT

  EcoRI    SmaI    XhoI        NdeI    NcoI    BamHI    NotI
GGA ATT CCC CGG GCT CGA GAA CAT ATG GCC ATG GGG ATC CGC GGC CGC

      HpaI          SalI        SacI
AAT TGT TAA CAG ATC CGT CGA CGA GCT CGC TA (530)
```

FIG. 3

CONSTRUCTION OF pGst-lox:

A

LINKER: C ATG GCT ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TG (SEQ ID NO: 3)
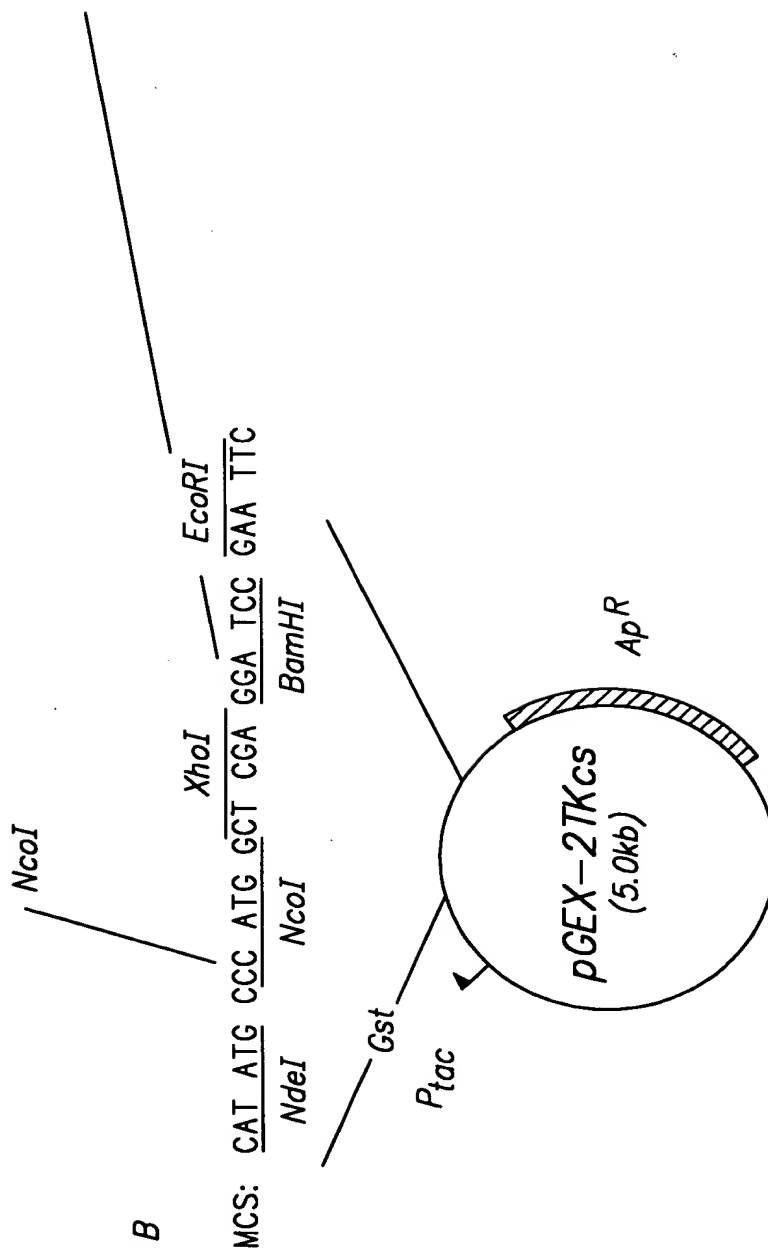　　　　　CGA TAT TGA AGC ATA TCG TAT GTA ATA TGC TTC AAT AC CTAG (SEQ ID NO: 4)

<u>NcoI</u>

<u>XhoI</u>　<u>EcoRI</u>
<u>BamHI</u>

B

MCS: CAT ATG CCC ATG GCT CGA GGA TCC GAA TTC
　　　<u>NdeI</u>　<u>NcoI</u>　<u>XhoI</u>　<u>BamHI</u>

Gst

P_{tac}

pGEX-2TKcs
(5.0kb)

Ap^R

FIG. 4

CONSTRUCTION OF pVL1392-lox:

A

LINKER: GG CCG GAC GTC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TG (SEQ ID NO: 6)
C CTG CAG TAT TGA AGC ATA TCG TAT GTA ATA TGC TTC AAT AC CTAG (SEQ ID NO: 7)

NotI   BamHI
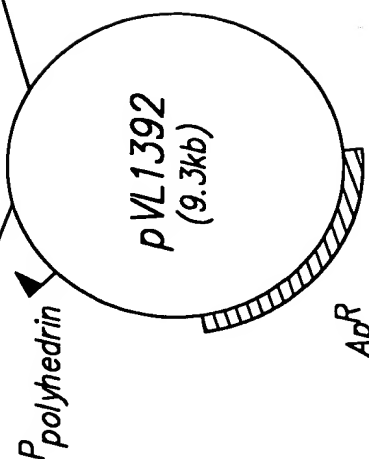
B

MCS: BglII/PstI/**NotI**/XmaI/EcoRI/XbaI/SmaI/**BamHI**

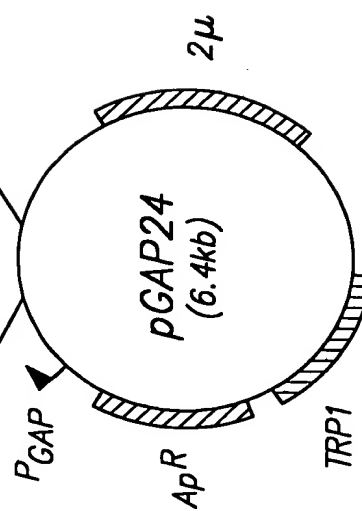$P_{polyhedrin}$

pVL1392
(9.3kb)

Ap^R

FIG. 5

CONSTRUCTION OF pGAP24-lox:

A

LINKER: T CGA GAC GTC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TGC (SEQ ID NO: 8)
        CTG CAG TAT TGA AGC ATA TCG TAT GTA ATA TGC TTC AAT ACG CCGG (SEQ ID NO: 9)

XhoI   NotI

B

MCS: **XhoI**/BclI/**NotI**/EagI/StyI/AflII

pGAP24
(6.4kb)

P_GAP

Ap^R

TRP1

2µ

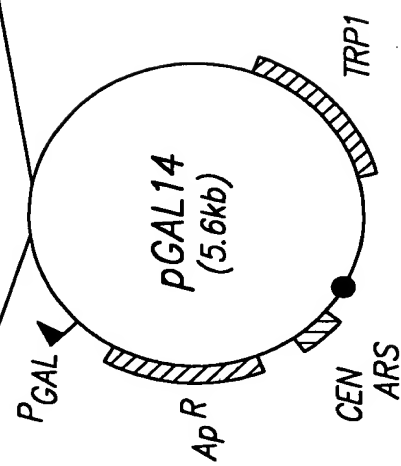# FIG. 6

CONSTRUCTION OF pGAL14-lox:

A

LINKER: T CGA GAC GTC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TGC (SEQ ID NO: 8)
CTG CAG TAT TGA AGC ATA TCG TAT GTA ATA TGC TTC AAT ACG CCGG (SEQ ID NO: 9)

XhoI

NotI

B

MCS: **Sal**I/ClaI/PstI/SmaI/XmaI/SpeI/**Not**I/EagI/SacII/SacI

FIG. 7

FIG. 11

FIG. 9B

FIG. 8

pB

Xho I IoxP Ori Bgl II

ApR

+

pA

Not I IoxP

OriR

KnR

Bgl II

Gst-Cre →

pAB

Not I IoxP Ori Bgl II

OriR

Bgl II

KnR

Xho I

IoxP

ApR

FIG. 9A

pGst-lox
(5.0kb)

Gst IoxP Pst I

Ptac

ApR

Ori

+

pUNI-Skp1
(2.8kb)

IoxP

OriR

Skp1

Pst I

KnR

Gst-Cre →

pGst-Skp1
(7.8kb)

Skp1

Ptac Gst IoxP

KnR

Pst I

OriR

IoxP

Pst I

ApR

Ori
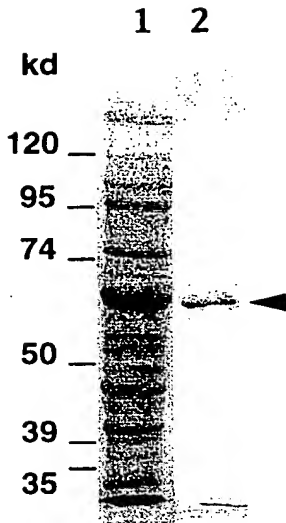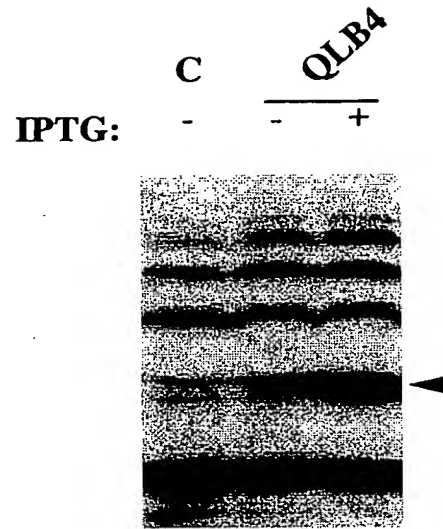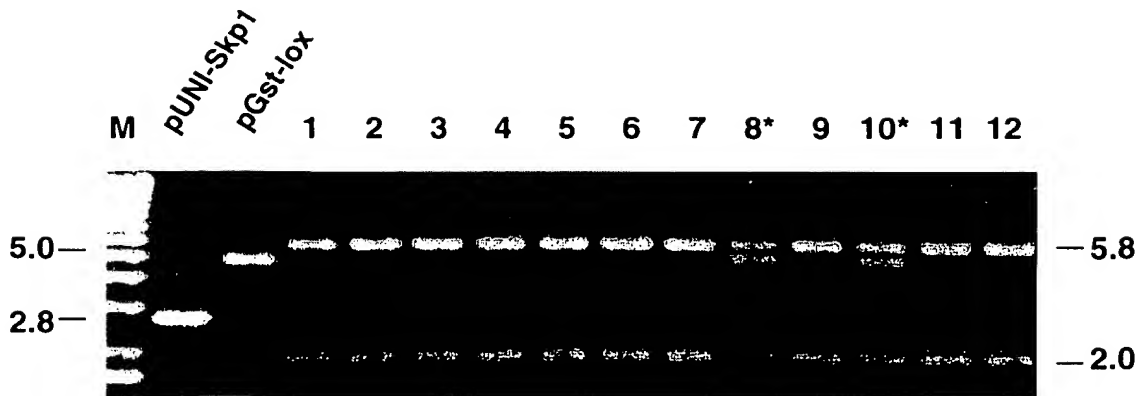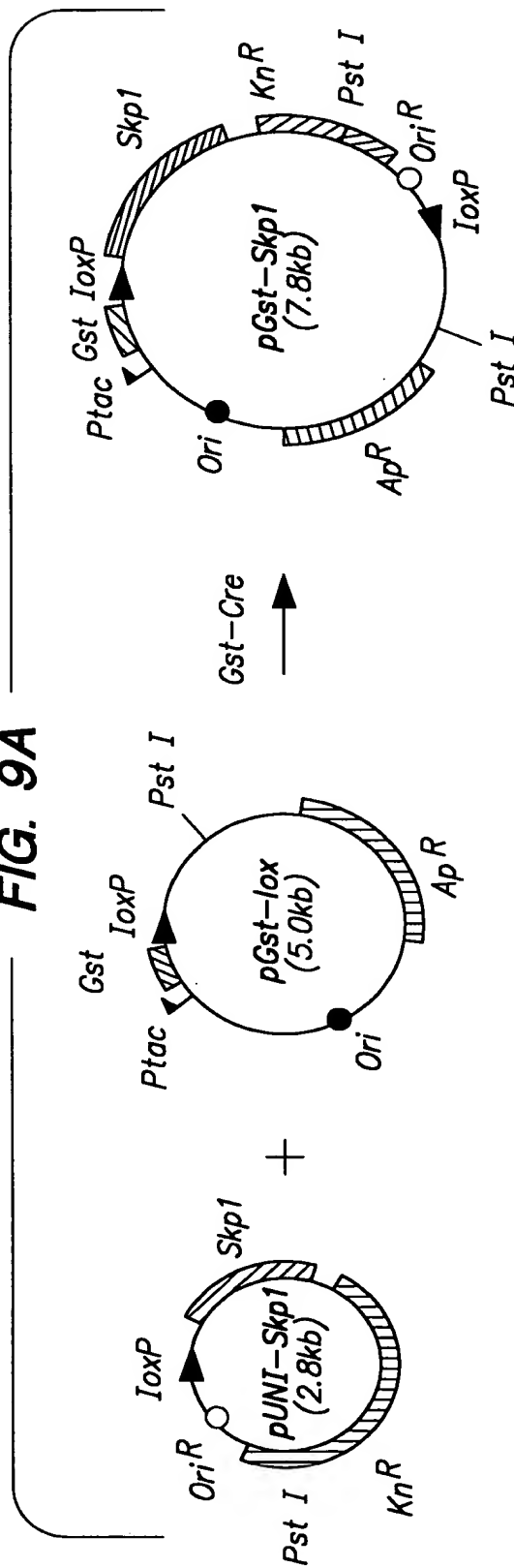
FIG. 10A

FIG. 10B

FIG. 12

FIG. 13

```
loxP:    A T A A C T T C G T A T A   G C A T A C A T   T A T A C G A A G T T A T (SEQ ID NO: 12)
         1 2 3 4 5 6 7 8 9 10111213                   13121110 9 8 7 6 5 4 3 2 1
                   T
                   C

loxP2:   A T A A C T T C G T A T A   G C A T A C A T   T A T A C G A A G T T A T (SEQ ID NO: 13)
         1 2 3 4 5 6 7 8 9 10111213                   13121110 9 8 7 6 5 4 3 2 1
                   T
                   C

loxP3:   A T A A C T T C G T A T A   G C A T A C A T   T A T A C G A A G T T A T (SEQ ID NO: 14)
         1 2 3 4 5 6 7 8 9 10111213                   13121110 9 8 7 6 5 4 3 2 1
                                                             T

loxP23:  A T A A C T T C G T A T A   G C A T A C A T   T A T A C G A A G T T A T (SEQ ID NO: 15)
         1 2 3 4 5 6 7 8 9 10111213                   13121110 9 8 7 6 5 4 3 2 1
                   T                                         T
                   C
```
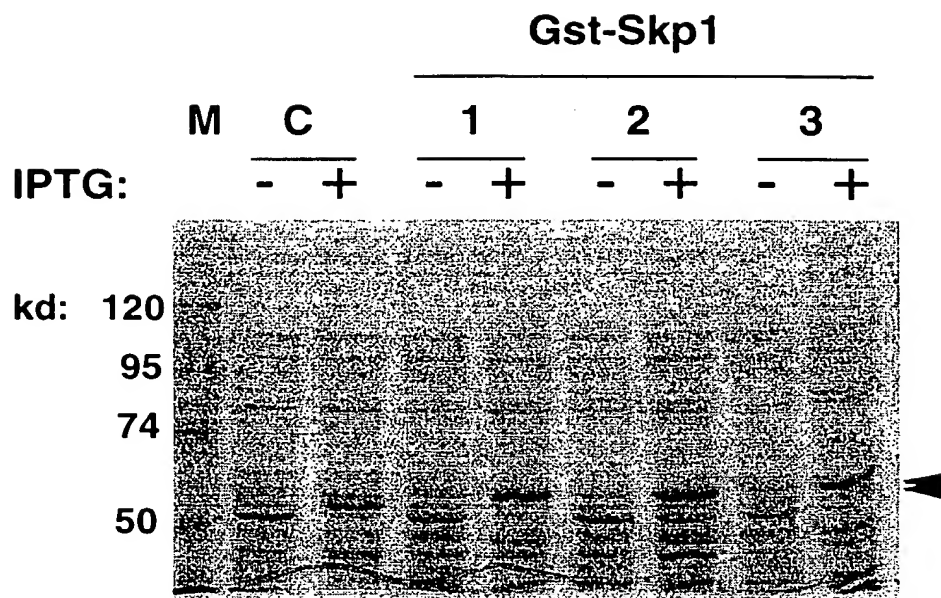
FIG. 14

FIG. 15

GST−Cre (µg)	NUMBER OF Ap^R TRANSFORMANTS	NUMBER OF Kn^R TRANSFORMANTS	Kn^R/Ap^R (%)
0	4.0×10^5	0	0
0.02	3.0×10^5	231	0.1
0.04	2.3×10^5	406	0.2
0.06	2.4×10^5	868	0.4
0.08	3.3×10^5	1,336	0.4
0.10	6.0×10^4	594	1.0
0.20	7.8×10^4	580	0.7
0.40	5.8×10^4	1,910	3.3
0.60	9.2×10^4	10,750	11.7
0.80	3.1×10^5	28,660	9.2
1.00	1.0×10^5	16,840	16.8

GST–Skp1   GST–lox–Skp1

IPTG: − +   − +   − +   − +

1   2   3   4   5   6   7   8
coomassie

FIG. 16A

GST–Skp1   GST–lox–Skp1

IPTG: − +   − +   − +   − +

1   2   3   4   5   6   7   8
western

FIG. 16B

Control   Myc3–Rnr4   Control   Myc3–lox–Rad53

− loxP loxH

1   2   3   4   5   6
yeast

FIG. 17

FIG.
SUBCLASS

APPL.
BY
DRAFTS

GST-Rad53
GST-lox-Rad53
Control
Myc3-lox-Rad53
Control
HA3-lox-Rad53

Control
HA3-lox-F3

1 2 3 4 5 6

insect cell

FIG. 18

1   2

mammalian
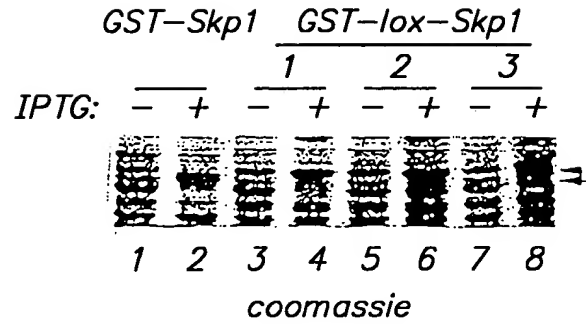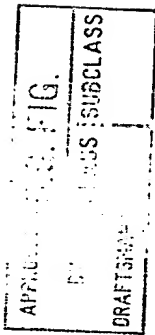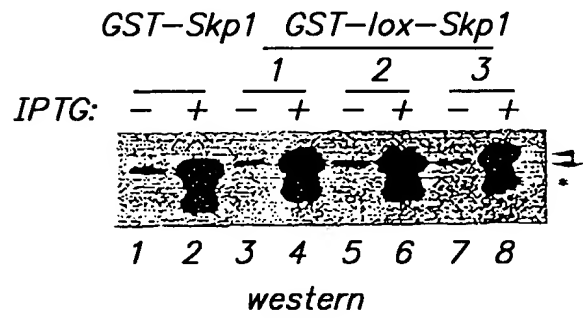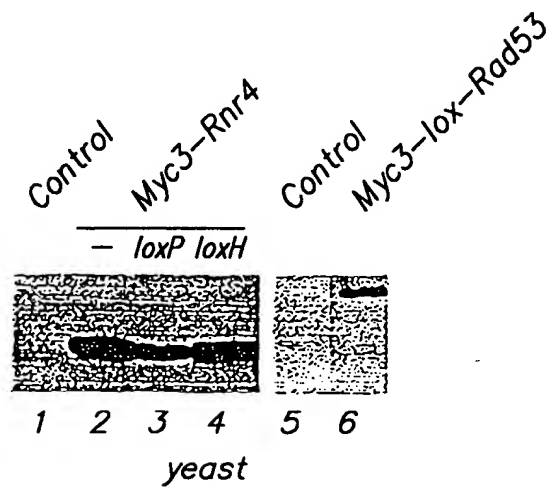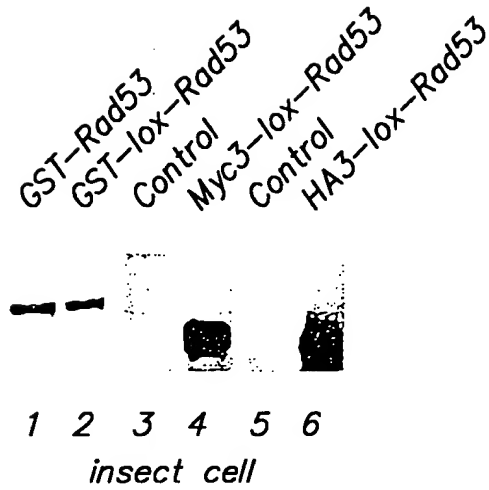
FIG. 19

FIG. 21

Pvu II restriction analysis of recombinant plasmids made by one-step POT

M P1 P2 I 1 2 3 4 5 6 7 8 9 10

FIG. 20

FIG. 22A

FIG. 22B

FIG. 22C
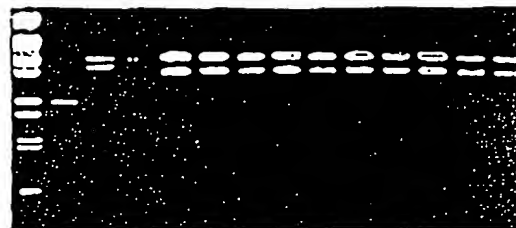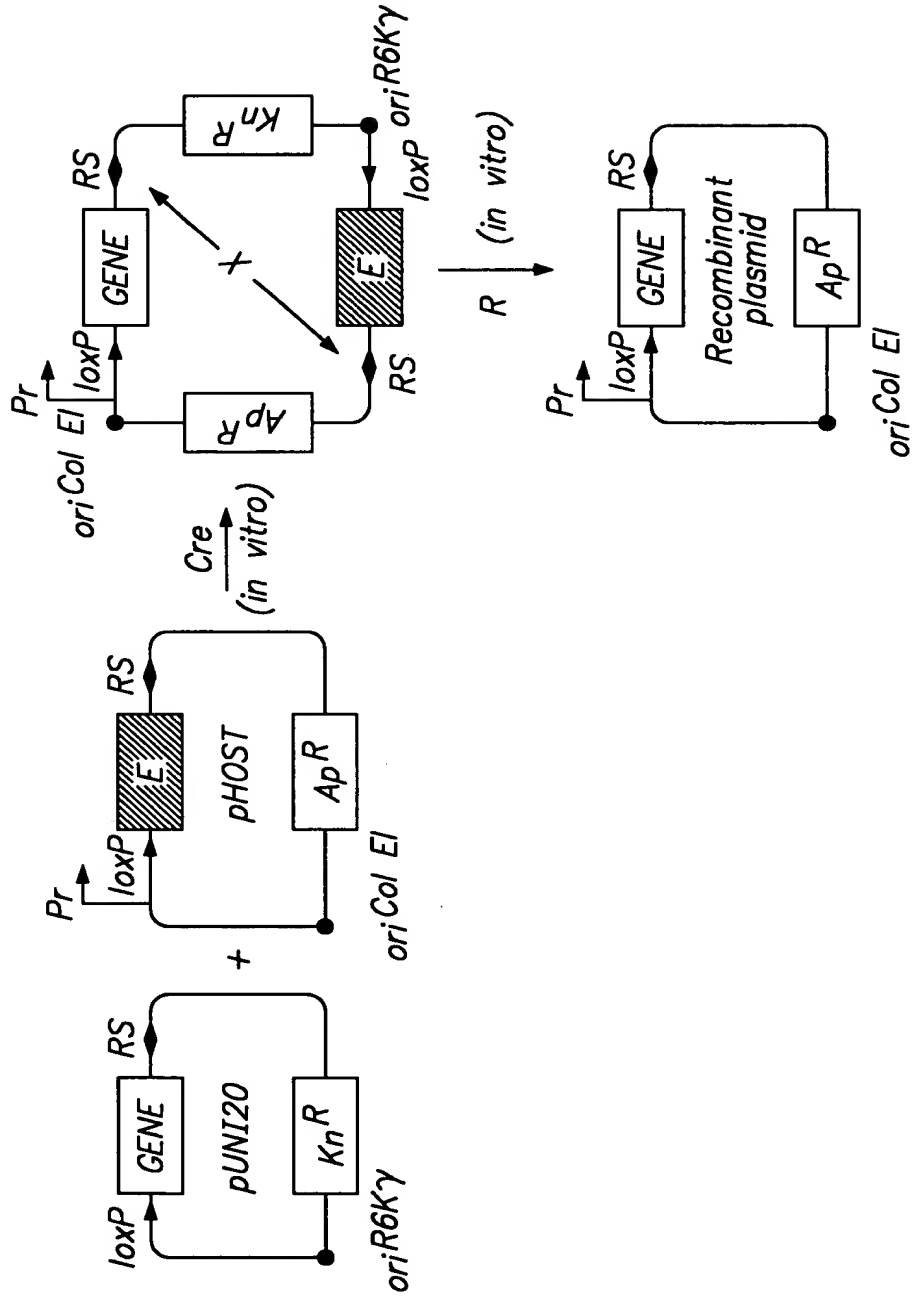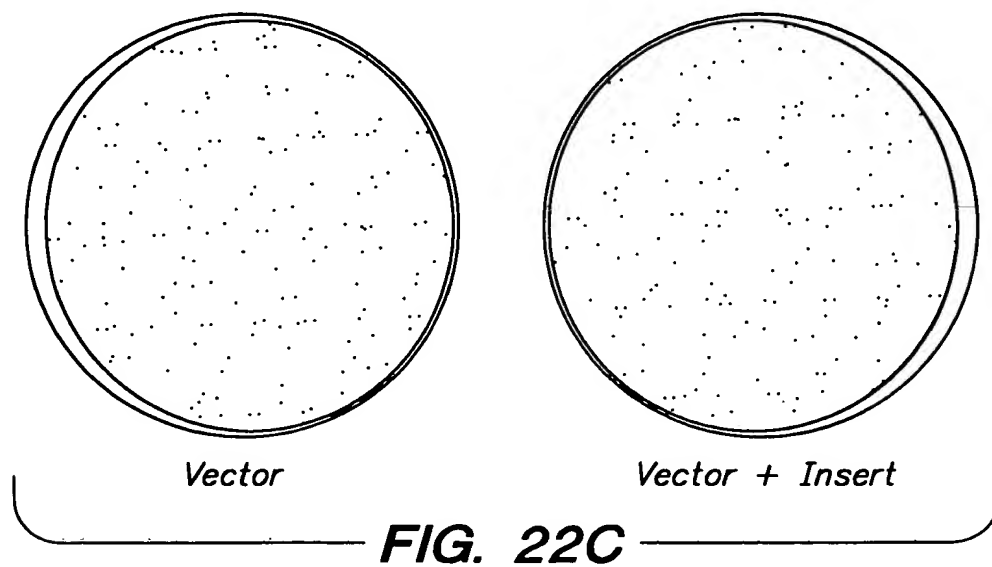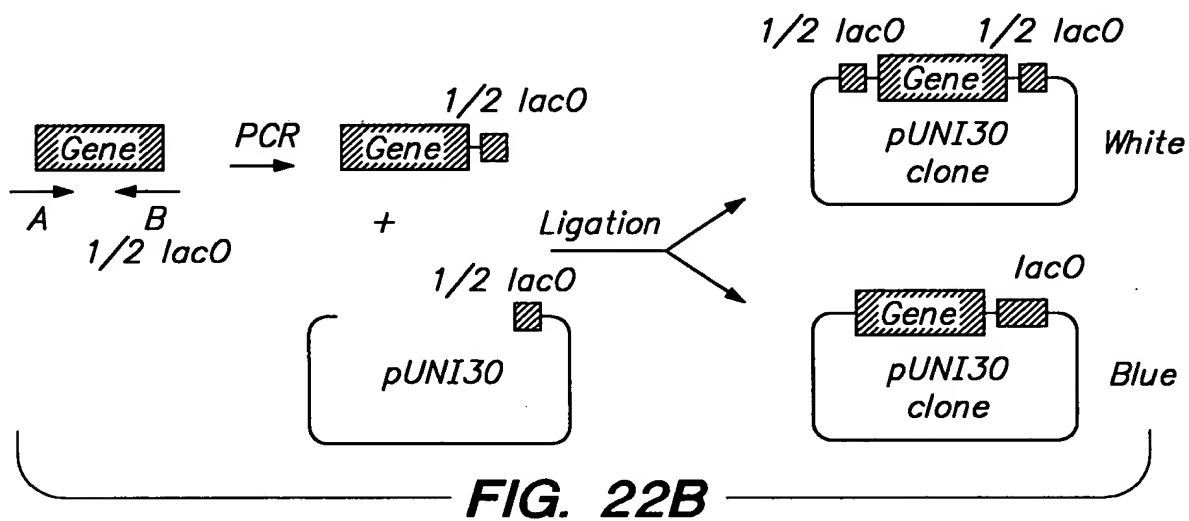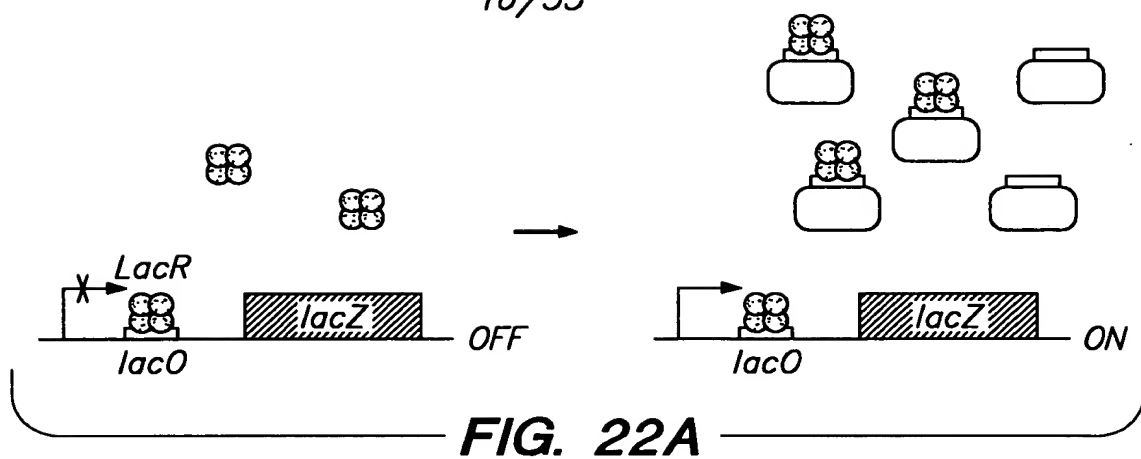
FIG. 23A
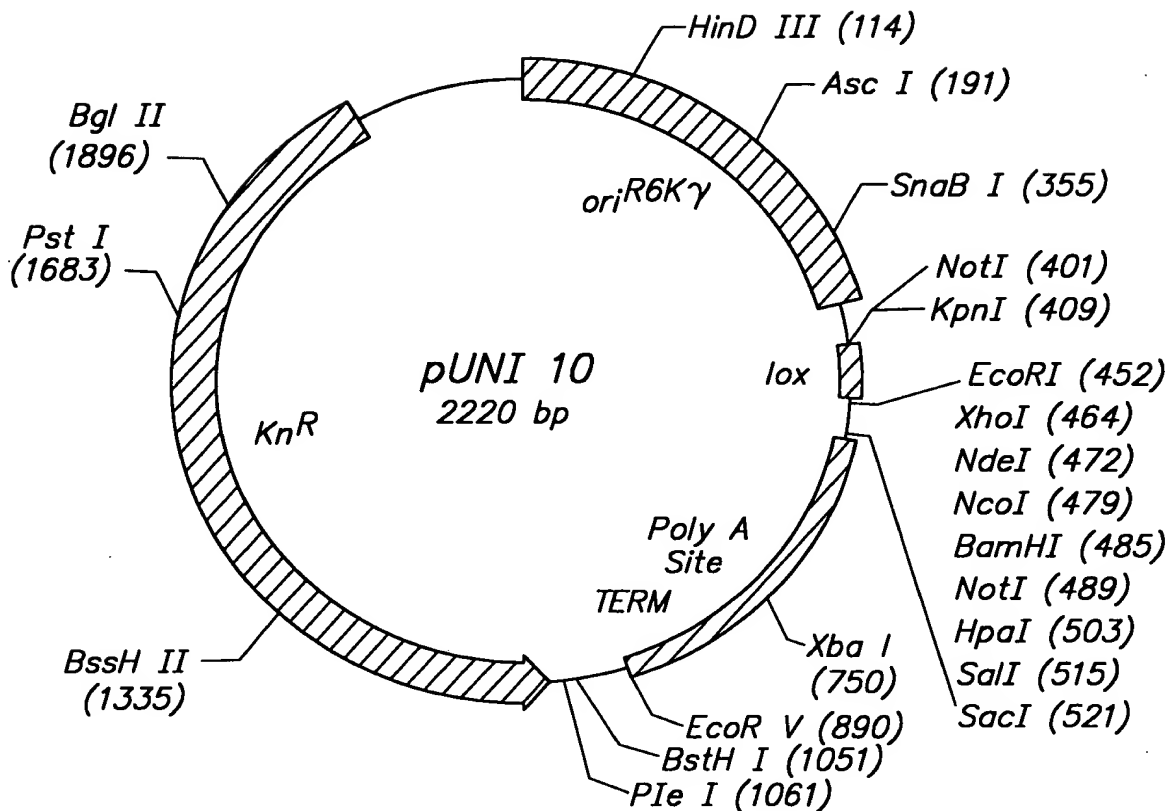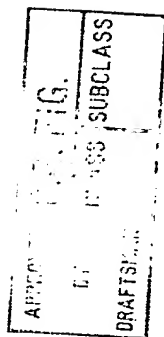
pUNI 10 POLYLINKER SEQUENCE

(401) NotI	KpnI	LOX
GC GGC CGC	GGT ACC	ATA ACT TCG TAT AGC ATA CAT TAT ACG A

	EcoRI	SmaI	XhoI	NdeI	NcoI
AG TTA TCT	GGA ATT	CCC CGG	GCT CGA GAA	CAT ATG	GCC ATG G

BamHI	NotI	HpaI	SalI	Sac I (530)
GG ATC CGC	GGC CGC	AAT TGT TAA CAG ATC	CGT CGA	CGA GCT

FIG. 23B

Nbe I (37)
Kpn I (357)
Polylinker (200–246)
Sal I (306)
Sac I (312)

Bgl II (2485)
Pst I (2272)

Res   lox   RS

BssH II
(1924)

KnR

Poly A
Site

TERM

pUNI 20
2490 bp

Xba I (541)

EcoR V (681)
Apa I (743)

ori R6Kγ

HinD III (862)

BstB I (1640)
MIa I (1634)

fI ori

SnaB I (1104)

Spe I (1149)
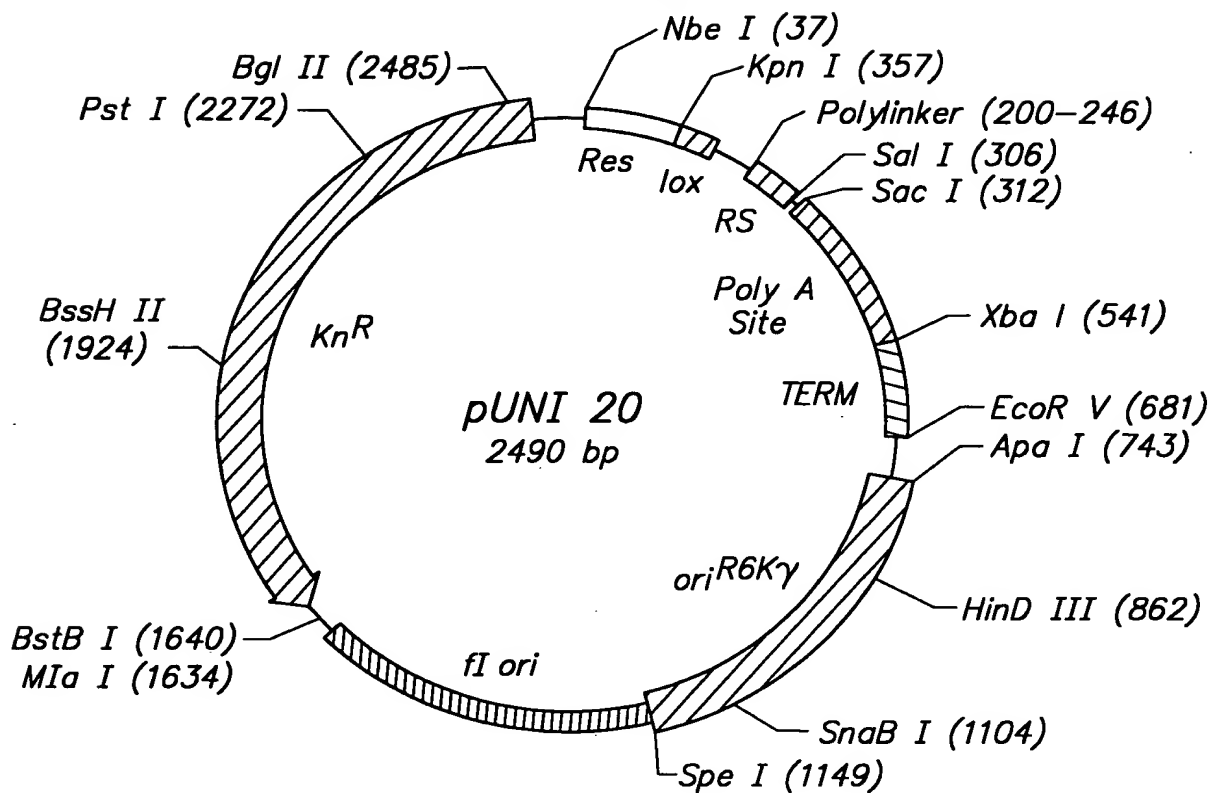
pUNI 20 POLYLINKER SEQUENCE

<u>(157) KpnI</u>_____<u>LOX</u>_____
GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA T

___<u>EcoR I</u>___<u>SmaI</u>___<u>XhoI</u>_____<u>Nde I</u>____<u>Nco I</u>___<u>BamHI</u>
CT GGA ATT CCC CGG GCT CGA GAA CAT ATG GCC ATG GGG ATC

<u>Not I (246)</u>
CGC GGC CGC

FIG. 23C

pUNI 30
2326 bp

Bgl II (2321)
Pst I (2808)
KpnI(37)
Polylinker (80–155)
lox
lacO
Xba I (377)
BssH II (1760)
KnR
Poly A Site
TERM
EcoR V (517)
Apa I (579)
ori R6Kγ
HinD III (698)
BstB I (1476)
MIa I (1470)
fI ori
SnaB I (939)
Spe I (985)
Ssp I (1097)
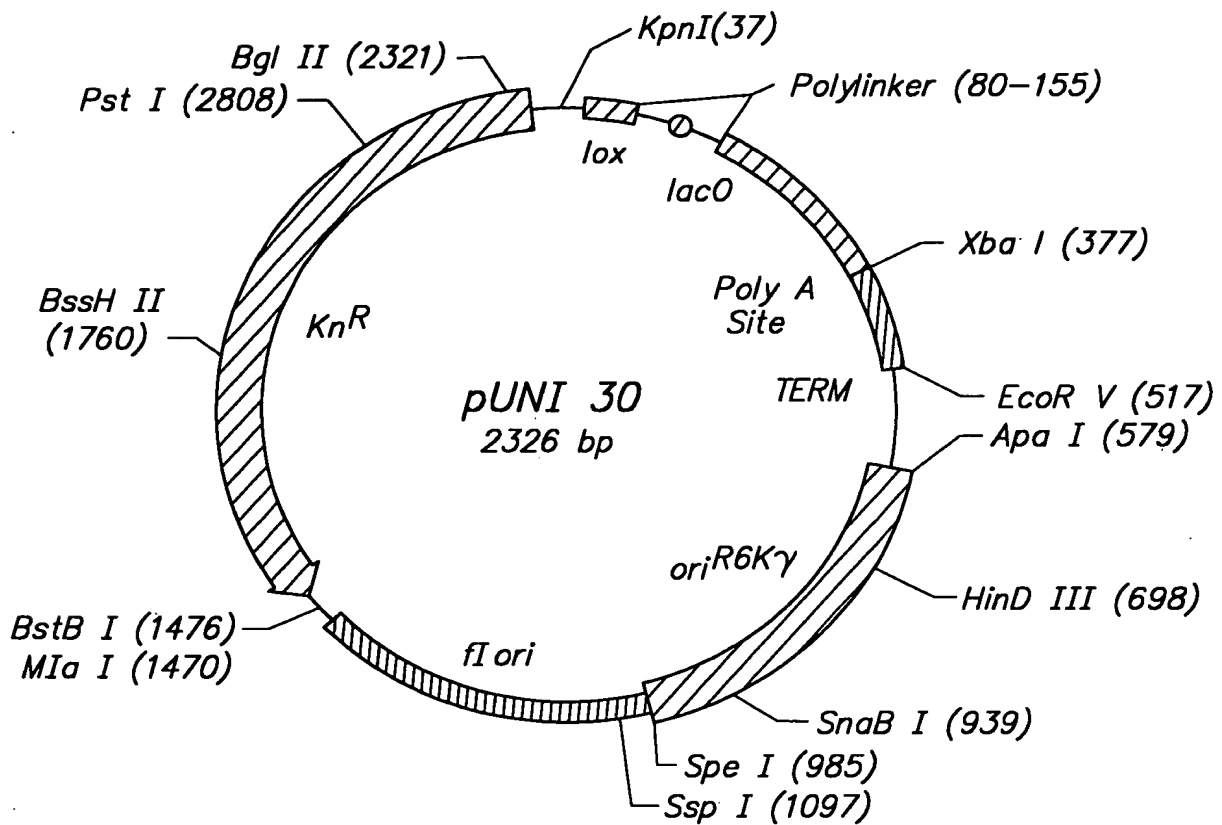
pUNI 30 POLYLINKER SEQUENCE

<u>(37) KpnI</u>   LOX

GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TC

<u>EcoR I</u>   <u>SmaI</u>   <u>XhoI</u>   <u>EcoIIIII</u>

T GGA ATT CCC CGG GCT CGA GCC AGT CCA GCG CTC ACA ATT

<u>half lacO</u>

<u>Not I</u>   <u>HpaI</u>   <u>Sal I</u> <u>SacI (155)</u>

GCG GGC GCA ATT GTT AAC AGA TCC GTC GAC GAG CTC GC

<u>MunI</u>
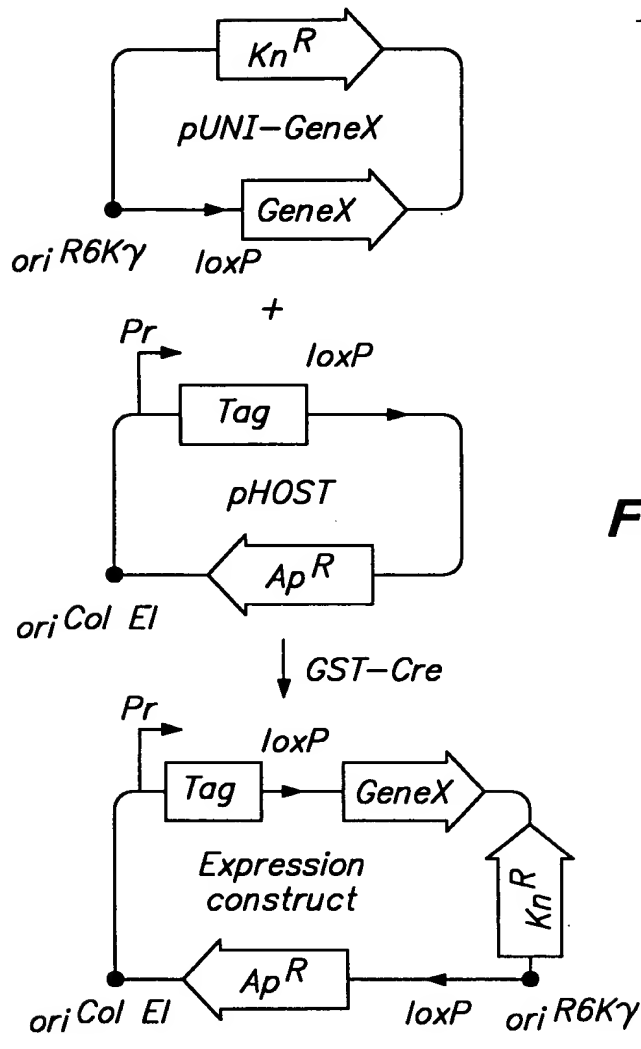
FIG. 24
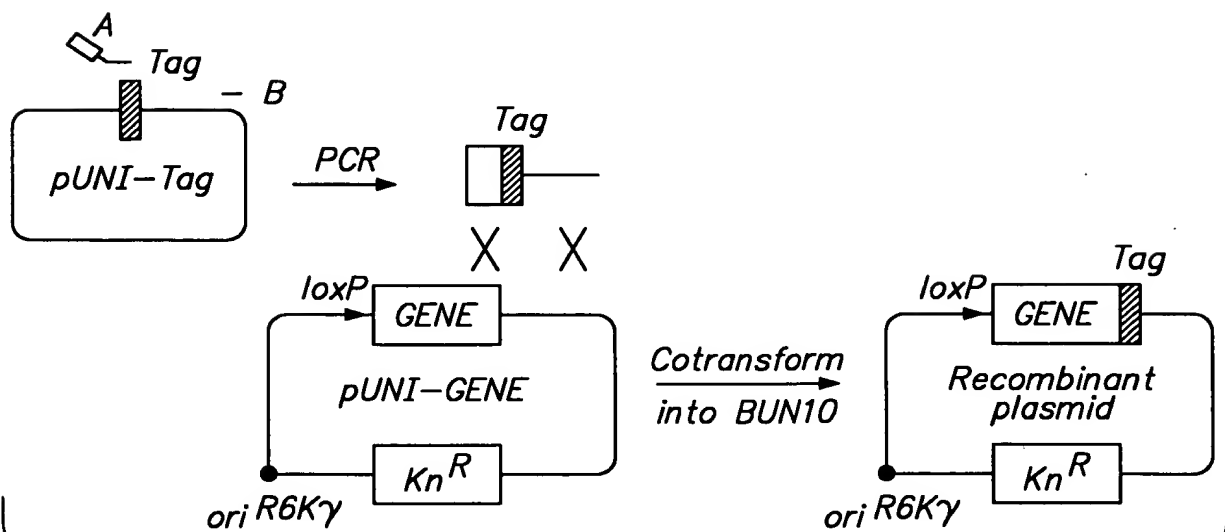
FIG. 25

FIG. 26A-1

SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATTCTGTCA GCCGTTAAGT GTTCCTGTGT CACTGAAAAT TGCTTTGAGA GGCTCTAAGG
60

GCTTCTCAGT GCGTTACATC CCTGGCTTGT TGTCCACAAC CGTTAAACCT TAAAAGCTTT
120

AAAAGCCTTA TATATTCTTT TTTTTCTTAT AAAACTTAAA ACCTTAGAGG CTATTTAAGT
180

TGCTGATTTA TATTAATTTT ATTGTTCAAA CATGAGAGCT TAGTACGTGA AACATGAGAG
240

CTTAGTACGT TAGCCATGAG AGCTTAGTAC GTTAGCCATG AGGGTTTAGT TCGTTAAACA
300

TGAGAGCTTA GTACGTTAAA CATGAGAGCT TAGTACGTGA AACATGAGAG CTTAGTACGT
360

ACTATCAACA GGTTGAACTG CTGATCAACA GATCCCTCTAC GCGGCCGCGG TACCATAACT
420

TCGTATAGCA TACATTATAC GAAGTTATCT GGAATTCCCC GGGCTCGAGA ACATATGGCC
480

ATGGGGATCC GCGGCCGCAA TTGTTAACAG ATCCGTCGAC GAGCTCGCTA TCAGCCTCGA
540

FIG. 26A-2

CTGTGCCTTC TAGTTGCCAG CCATCTGTTG TTTGCCCCTC CCCCGTGCCT TCCTTGACCC
600

TGGAAGGTGC CACTCCCACT GTCCTTTCCT AATAAAATGA GGAAATTGCA TCGCATTGTC
660

TGAGTAGGTG TCATTCTATT CTGGGGGGTG GGGTGGGGCA GGACAGCAAG GGGGAGGATT
720

GGGAAGACAA TAGCAGGCAT GCTGGGGATT CTAGAAGATC CGGCTGCTAA CAAAGCCCGA
780

AAGGAAGCTG AGTTGGCTGC TGCCACCGCT GAGCAATAAC TAGCATAACC CCTTGGGGCC
840

TCTAAACGGG TCTTGAGGGG TTTTTTGCTG AAAGGAGGAA CTATATCCGG ATATCCCGGG
900

GTGGGCGAAG AACTCCAGCA TGAGATCCCC GCGCTGGAGG ATCATCCAGC CGGCGTCCCG
960

GAAAACGATT CCGAAGCCCA ACCTTTCATA GAAGGCGGCG GTGGAATCGA AATCTCGTGA
1020

TGGCAGGTTG GGCGTCGCTT GGTCGGTCAT TTCGAACCCC AGAGTCCCGC TCAGAAGAAC
1080

FIG. 26A-3

TCGTCAAGAA GGGCGATAGAA GGCGATGCGC TGCGAATCGG GAGCGGCCGAT ACCGTAAAGC
1140

ACGAGGAAGC GGTCAGCCCA TTCGCCGCCA AGCTCTTCAG CAATATCACG GGTAGCCAAC
1200

GCTATGTCCT GATAGCGGTC CGCCACACCC AGCCGGCCAC AGTCGATGAA TCCAGAAAAG
1260

CGGCCATTTT CCACCATGAT ATTCGGCAAG CAGGCATCGC CATGGGTCAC GACGAGATCC
1320

TCGCCGTCGG GCATGCGCGC CTTGAGCCTG GCGAACAGTT CGGCTGGCGC GAGCCCCTGA
1380

TGCTCTTCGT CCAGATCATC CTGATCGACA AGACCGGCTT CCATCCGAGT ACGTGCTCGC
1440

TCGATGCGAT GTTTCGCTTG GTGGTCGAAT GGGCAGGTAG CCGGATCAAG CGTATGCAGC
1500

CGCCGCATTG CATCAGCCAT GATGGATACT TTCTCGGCAG GAGCAAGGTG AGATGACAGG
1560

AGATCCTGCC CCGGCACTTC GCCCAATAGC AGCCAGTCCC TTCCCGCTTC AGTGACAACG
1620

TCGAGCACAG CTGGCCAAGG AACGCCCGTC GTGGCCAGCC ACGATAGCCG CGCTGCCTCG
1680

FIG. 26A-4

```
TCCTGCAGTT CATTCAGGGC ACCGGACAGG TCGGTCTTGA CAAAAAGAAC CGGGGCCCC
1740

TGCGCTGACA GCCGGAACAC GGCGGCATCA GAGCAGCCGA TTGTCTGTTG TGCCCAGTCA
1800

TAGCCGAATA GCCTCTCCAC CCAAGCGGCC GGAGAACCTG CGTGCAATCC ATCTTGTTCA
1860

ATCATGCGAA ACGATCCTCA TCCTGTCTCT TGATCAGATC TTGATCCCCT GCGGCCATCAG
1920

ATCCTTGGCG GCAAGAAAGC CATCCAGTT ACTTTGCAGG GCTTCCCAAC CTTACCAGAG
1980

GGCGCCCCAG CTGGCAATTC CGGTTCGCTT GCTGTCCATA AAACCGCCCA GTCTAGCTAT
2040

CGCCATGTAA GCCCACTGCA AGCTACCTGC TTTCTCTTTG CGCTTGCGTT TTCCCTTGTC
2100

CAGATAGCCC AGTAGCTGAC ATTCATCCGG GGTCAGCACC GTTTCTGCGGG ACTGGCTTTC
2160

TACGTGTTCC GCTTCCTTTA GCAGCCCTTG CGCCCTGAGT GCTTGCGGCA GCGTGAAGCT
2220
```
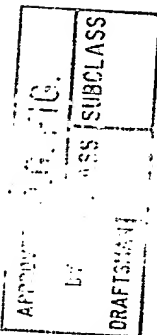
FIG. 26B-1

SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG TCC CCT ATA CTA GGT TAT TGG AAA ATT AAG GGC CTT GTG CAA CCC
48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1   5   10   15

ACT CGA CTT CTT TTG GAA TAT CTT GAA GAA AAA TAT GAA GAG CAT TTG
96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
        20   25   30

TAT GAG CGC GAT GAA GGT GAT AAA TGG CGA AAC AAA AAG TTT GAA TTG
144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35   40   45

GGT TTG GAG TTT CCC AAT CTT CCT TAT TAT ATT GAT GGT GAT GTT AAA
192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50   55   60

TTA ACA CAG TCT ATG GCC ATC ATA CGT TAT ATA GCT GAC AAG CAC AAC
240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65   70   75   80

FIG. 26B-2

ATG TTG GGT TGT CCA AAA GAG CGT GCA GAG ATT TCA ATG CTT GAA
288
Met Leu Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
          85   90   95

GGA GCG GTT TTG GAT ATT AGA TAC GGT GTT TCG AGA ATT GCA TAT AGT
336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
              100   105   110

AAA GAC TTT GAA ACT CTC AAA GTT GAT TTT CTT AGC AAG CTA CCT GAA
384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
          115   120   125

ATG CTG AAA ATG TTC GAA GAT CGT TTA TGT CAT AAA ACA TAT TTA AAT
432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
          130   135   140

GGT GAT CAT GTA ACC CAT CCT GAC TTC ATG TTG TAT GAC GCT CTT GAT
480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
          145   150   155   160

FIG. 26B-3

```
GTT GTT TTA TAC ATG GAC CCA ATG TGC CTG GAT GCG TTC CCA AAA TTA
528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
              165             170             175

GTT TGT TTT AAA AAA CGT ATT GAA GCT ATC CCA CAA ATT GAT AAG TAC
576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
          180             185             190

TTG AAA TCC AGC AAG TAT ATA GCA TGG CCT TTG CAG GGC TGG CAA GCC
624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
      195             200             205

ACG TTT GGT GGT GGC GAC CAT CCT CCA AAA TCG GAT CTG GTT CCG CGT
672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
      210             215             220

GGA TCT CGT CGT GCA TCT GTT GGA TCG CAT ATG CCC ATG GCC AAT TTA
720
Gly Ser Arg Arg Ala Ser Val Gly Ser His Met Pro Met Ala Asn Leu
      225             230             235             240

CTG ACC GTA CAC CAA AAT TTG CCT GCA TTA CCG GTC GAT GCA ACG AGT
768
Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val Asp Ala Thr Ser
      245             250             255
```
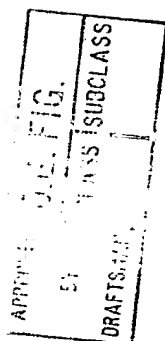
FIG. 26B-4

```
GAT GAG GTT CGC AAG AAC CTG ATG GAC ATG TTC AGG GAT CGC CAG GCG
816
Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg Asp Arg Gln Ala
            260            265            270

TTT TCT GAG CAT ACC TGG AAA ATG CTT CTG TCC GTT TGC CGG TCG TGG
864
Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val Cys Arg Ser Trp
            275            280            285

GCG GCA TGG TGC AAG TTG AAT AAC CGG AAA TGG TTT CCC GCA GAA CCT
912
Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe Pro Ala Glu Pro
            290            295            300

GAA GAT GTT CGC GAT TAT CTT CTA TAT CTT CAG GCG CGC GGT CTG GCA
960
Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala Arg Gly Leu Ala
            305            310            315            320

GTA AAA ACT ATC CAG CAA CAT TTG GGC CAG CTA AAC ATG CTT CAT CGT
1008
Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn Met Leu His Arg
            325            330            335

CGG TCC GGG CTG CCA CGA CCA AGT GAC AGC AAT GCT GTT TCA CTG GTT
1056
Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala Val Ser Leu Val
            340            345            350
```
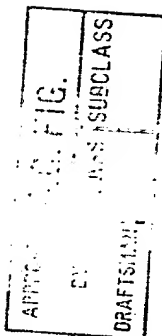
FIG. 26B-5

```
1104  ATG CGG CGG ATC CGA AAA GAA AAC GTT GAT GCC GGT GAA CGT GCA AAA
      Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly Glu Arg Ala Lys
                    355              360              365

1152  CAG GCT CTA GCG TTC GAA CGC ACT GAT TTC GAC CAG GTT CGT TCA CTC
      Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln Val Arg Ser Leu
              370              375              380

1200  ATG GAA AAT AGC GAT CGC TGC CAG GAT ATA CGT AAT CTG GCA TTT CTG
      Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe Leu
              385              390              395              400

1248  GGG ATT GCT TAT AAC ACC CTG TTA CGT ATA GCC GAA ATT GCC AGG ATC
      Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg Ile
              405              410              415

1296  AGG GTT AAA GAT ATC TCA CGT ACT GAC GGT GGG AGA ATG TTA ATC CAT
      Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg Met Leu Ile His
              420              425              430

1344  ATT GGC AGA ACG AAA ACG CTG GTT AGC ACC GCA GGT GTA GAG AAG GCA
      Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly Val Glu Lys Ala
              435              440              445
```
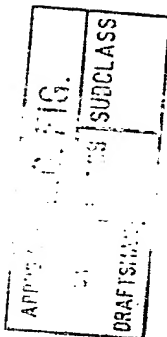
FIG. 26B-6

```
CTT AGC CTG GGG GTA ACT AAA CTG GTC GAG CGA TGG ATT TCC GTC TCT
1392
Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp Ile Ser Val Ser
          450                     455                     460

GGT GTA GCT GAT GAT CCG AAT AAC TAC CTG TTT TGC CGG GTC AGA AAA
1440
Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg Lys
465                     470                     475                 480

AAT GGT GTT GCC GCG CCA TCT GCC ACC AGC CAG CTA TCA ACT CGC GCC
1488
Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg Ala
      485                     490                     495

CTG GAA GGG ATT TTT GAA GCA ACT CAT CGA TTG ATT TAC GGC GCT AAG
1536
Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile Tyr Gly Ala Lys
              500                     505                     510

GAT GAC TCT GGT CAG AGA TAC CTG GCC TGG TCT GGA CAC AGT GCC CGT
1584
Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly His Ser Ala Arg
          515                     520                     525

GTC GGA GCC GCG CGA GAT ATG GCC CGC GCT GGA GTT TCA ATA CCG GAG
1632
Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val Ser Ile Pro Glu
      530                     535                     540
```

FIG. 26B-7

ATC ATG CAA GCT GGT GGC TGG ACC AAT GTA AAT ATT GTC ATG AAC TAT
1680
Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile Val Met Asn Tyr
545   550   555   560

ATC CGT AAC CTG GAT AGT GAA ACA GGG GCA ATG GTG CGC CTG CTG GAA
1728
Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val Arg Leu Leu Glu
                   565   570   575

GAT GGC GAT TAG
1740
Asp Gly Asp
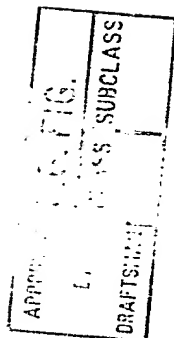
FIG. 26C-1

SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1   5   10   15

Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
        20   25   30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35   40   45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50   55   60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65   70   75   80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
            85   90   95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100   105   110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115   120   125

FIG. 26C-2

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130   135   140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145   150   155   160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165   170   175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180   185   190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195   200   205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210   215   220

Gly Ser Arg Arg Ala Ser Val Gly Ser His Met Pro Met Ala Asn Leu
225   230   235   240

Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val Asp Ala Thr Ser
245   250   255

Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg Asp Arg Gln Ala
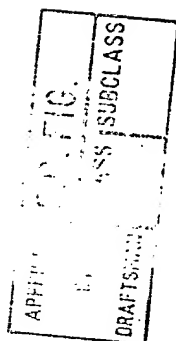260   265   270

FIG. 26C-3

```
Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val Cys Arg Ser Trp
                    275             280             285

Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe Pro Ala Glu Pro
            290             295             300

Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala Arg Gly Leu Ala
        305             310             315             320

Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn Met Leu His Arg
            325             330             335

Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala Val Ser Leu Val
            340             345             350

Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly Glu Arg Ala Lys
            355             360             365

Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln Val Arg Ser Leu
            370             375             380

Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe Leu
        385             390             395             400

Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg Ile
            405             410             415

Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg Met Leu Ile His
            420             425             430
```

FIG. 26C-4

Ile Gly Arg Thr Lys Thr Ala Gly Val Ser Thr Leu Val Ser Thr Ala Gly Val Glu Lys Ala
435   440   445

Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp Ile Ser Val Ser
450   455   460

Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg Lys
465   470   475   480

Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg Ala
485   490   495

Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile Tyr Gly Ala Lys
500   505   510

Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly His Ser Ala Arg
515   520   525

Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val Ser Ile Pro Glu
530   535   540

Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile Val Met Asn Tyr
545   550   555   560

Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val Arg Leu Leu Glu
565   570   575

Asp Gly Asp